W30082 W38705

Rat persephin. GDN S. pneumoniae phos

ALIGNMENTS

OM protein protein search, using sw model

Run on: September 17, 1999, 03:08:16; 6 ; Search time 64.1 Seconds
(without alignments)
11.086 million cell updates/sec

Perfect score: US-09-037-657-32 139

Sequence:

BLOSUM62

MVLASSTTSIHTMLLLLLMLFHLGLQASIS 30

Database : A\_Geneseq\_36:\*

188963 segs, 23686106 residues

Searched: Scoring table:

score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution. Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

## SUMMARIES

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e. Cellul	မှ	Peripheral nervous	٠,	00000		BV0+03+0	Y .	beta	Human high affinit	ORF 8 gene product	no acto			9	BAV3 ORF2 product.	N-terminal of 48 k	odomi	T Sharacana		beet beta-	e melanocorti	Mouse melanocyte s	:	e won a. Mer	D MCU-D	CA COLUMN NOT	IK1 protei		Human secreted pro	E. coli antibiotic		E. COLL ANTIDIOTIC	TOCATI	Particular services	101010	ein coupled	73	Partial human 7-tr	Human 7-transmembr	thurin	Anther speciic pro	111a		ncr con	-		ע	Seguence encoded b	ripti
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Murine IL-3 signal sequence. LERK; ligand for eph-related kinase; receptor protein tyrosine kinase; cel

(first entry)

signal peptide; protein secretion.

kinase; cell proliferation;
survival; nerve cell; interleukin-3;

.0638 standard; Peptide; 30

\$

WPI; 97-132632/12.
Nucleic acid mol. encoding ligand for eph-related kinase for treatment of, pref. neuronal, cells to increase surviproliferation and differentiation example 3; Page 30; 71pp; English.

Nicola NA;

AMRAD OPERATIONS PTY LTD

)5-FEB-1996;

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                                                                               Query Match
Best Local Similarity
Matches 30; Conserv
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The cDNA is derived from messenger RNA isolated from a mouse T-cell line after activation with concanavalin A. The cDNA was cloned by incorporation into a plasmid vector, which then transformed into E.coli. The plasmid vector also contained DNA segments from the SV40 virus, permitting expression of the cDNA after transfection into a mammalian host cell, such as monkey COS-7 cells. The polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SCHE) SCHERING CORP.
(DNAX-) DNAX RES INST MOLEC.
FOROTA T, Lee FD, Rennick DM, Arai KI;
RPI; 85-100349/17.
                                                                                                                                                                                                                 includes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50161 standard; Protein; 166 AA
                                                                                                                                                                                                                                                                                                                                                                                                          ew poly:peptide(s) having growth factor activities -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   equence
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                      1 MYLASSTTSIHTMLLLLLMLFHLGLQASIS 30
                                                                                                                                                                                                                                                                                                                                                                                             recombinant
MVLASSITSIHIMLILLIMLFHLGLQASIS 30
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encoded by cDNA clone exhibiting multi-lineage cellular
                                                                                                                                                                                             potential leader sequence of about 19 AAs. 166 AA;
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Pred. No. 7.2e-14;
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                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding animal haemopoietin receptor which interacts with interleukin-13 - useful to treat asthma, allergy or condition exacerbated by IgE production

Example 2; Page 56; 93pp; English.

Using PCR, a derivative of novel haemoprotein receptor NR4 CDNA was generated which encoded the interleukin-3 signal peptide (W09823) and an N-terminal FLAG epitope tag (W09824) preceding the mature coding region (Thr27-Pro424) of murine NR4 (see also W09821). The PCR product was cloned into the mammalian expression vector
                                                                                 Construct containing mature interleukin-13 binding protein. Therapeutic: II-3 mediated condition; allergy; asthma; diagnosis; autoimmune disease; antibody; immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-OCT-1995; AU-006135.
22-DCC-1995; AU-007276.
09-SEP-1996; AU-0072208.
(AMEA-) AMEAD OPERATIONS PTY LTD.
Hilton DJ. Metcalf D, Nicola NA,
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WO9715663-A1.
                                                        Homo sapiens. W09810638-A1.
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WPI; 97-259018/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-OCT-1995; AU-0068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interleukin-3 signal peptide.
Interleukin-3; IL-3; signal peptide; NR4; haemoprotein receptor;
Interleukin-13 receptor; cytokine; allergy; asthma; therapy.
10-SEP-1997; AU0591.
27-FEB-1997; AU-005374.
10-SEP-1996; AU-002262
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                                                                                                                                                          V56260 standard; Protein;
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MVLASSITSIHTMLLLLLMLFHLGLQASIS MYLASSITSIHIMLLLLLMLFHLGLQASIS

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Query Match Best Local S Matches 30

Similarity

100.0%; llarity 100.0%; Conservative

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Score 139; DB 1 Pred. No. le-14; Mismatches

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Matches 30; Conserv
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Example 14; Page 52-53; 69pp; English.

The II-13 binding protein and related therapeutic molecules can be used for the antagonism of at least one II-13 activity. They can be used for treating II-13 mediated conditions such as certain allergic conditions such as asthma or to inactivate locally administered II-13 after II-13 treatment. The products can also be used as diagnostic agents, e.g. for detecting autoimmune diseases. The antibodies can also be used for immunotherapy and may also be used as a diagnostic tool.

Sequence 359 AA;
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W55017;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AMRA-) AMRAD OPERATIONS PTY LTD.
Hilton DJ, Nicola NA, Simpson RJ,
e.g. for 
Sequence
                                 Claim 29(1); Page 54; 182pp; English.

The mouse IL3 signal sequence was used to study the expression of mouse NR6.1. NR6.1 is a form of NR6 a novel Haemopoletin receptor (HR).

Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis,
                                                                                                                                                                                                               WPI; 98-260970/23:
WPI; 98-260970/23:
New isolated haemopoletin receptor - used for developing products
for modulating proliferation, differentiation and survival of cells,
e.g. neuronal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse.
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Murine II3 signal sequence.
Haemopoietin receptor; cell
cell survival; therapeutic;
                                                                                                                                                                                                                                                                                                                                           11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS PTY LTD.
(DZIE/) DZIEGLEWSKA H E.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus sp.
W09811225-A2.
                                                                                                                                                                                                                                                                                                        (DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
                                                                                                                                                                                                                                                                                                                                                                                                                    19-MAR-1998
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No. 1.7e-13;
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                      cancers,
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Database : Searched: Scoring table:

Sequence: Perfect score: Title: Run on:

A70394 Sequence 24 A70393 Sequence 23 AF060868 Mus muscu AF139987 Mus muscu

AC004093 Mus muscu AC004155 Mus muscu

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AC003060 Mus muscu AF050157 Mus muscu AF100956 Mus muscu

Mouse BAC

Mus musculu M.musculus A70382 Sequence 12 A70384 Sequence 14 A70388 Sequence 18 AF059293 Homo sap1

A70398 Sequence A70386 Sequence A70392 Sequence AC003112 Human I

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A70408
94774683
A70408.1 GI:4774683
                                                                                                             unclassified.

1 (bases 1 to 11832)

Nicola, N.A., Fabri, L., Farley, A., Nash, A., Willson, T., Rakar, S., Zhang, J., Alexander, W., Hilton, D.J., Kojima, T., Maeda, M. and Kikuchi, Y.
                                                          A NOVEL HARMOPOISTIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME PATENT: WO 9811225-A 19-MAR-1998;
NICOLA NICOS ANTONY (AU)
Location/Qualifiers
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PAT

07-MAY-1999

A70390 Sequence 20 AC001230 Genomic s U14720 Mus musculu

AF136179 Mus muscu

AC003994 Mouse cos AC003066 Mus muscu AC0036507 Mus muscu AC005816 , complet AF109906 Mus muscu AC007049 , complet AC005992 Mus muscu

AC005818 , complet AC005302 Mus muscu AC003018 Mus muscu AC003489 Homo sap1 AC006945 Mus muscu AC003063 Mus muscu

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1 (bases 1 to 938)

Nicola, N.A., Fabri, L., Farley, A., Nas Zhang, J., Alexander, W., Hilton, D.J.,
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           Ω
          /translation="GTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGEPSGGPVRRELKQFGWLKKHAYCSSLSFLLYDQWRAWMQKSHKTRNQVGKLEACKGEACVGGKCAEEERDPGEQPPQHRTLLSKHRTRGSCPRADGVRREVRGSG"
a 245 c 272 g 178 t
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Kojima,T., Maeda,M. and
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Query Match Best Local S Matches 777

al Similarity 777; Conserv

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Score 737.2; DB 5; Pred. No. 1.8e-145; 0; Mismatches 28;

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             1 (bases 1 to 1930)
Nicola,N.A., Fabri/L., F
Zhang,J., Alexander,W.,
Kikuchi,Y.
                                                         unidentified unidentified
                                                unclassified.
   NOVEL HAEMOPOIETIN
                                                                                     GI:4774670
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 RECEPTOR AND GENETIC
                 ., Farley,A., Nash,A., Willson,T., R
W., Hilton,D.J., Kojima,T., Maeda,M.
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         tttaaataaataaaggagttgttcaggt 11787
                                                                                                               acca--gaggctgggcacaatgagctcccacaaccaccagctttggtccacatgatggtca
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                                                                                                 ACCATGAGGCTGGGGCACAATGAGCTCCCACAACCACAGCTTTGGTCCACATGATGGTCA
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                                                                                                                                                     GACCTGGÀGGCTCACCTGAATTGGAGCCCCTCTGTACCTATCTGGGCCAACAAAGAAACCT
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nilarity 96.2%;
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NICOS ANTONY (AU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="unidentified"
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623 c 561 g 37
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Pred. No. 1.6e-145;
0; Mismatches 28;
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	_	uterus NbHPU Homo sapiens cDNA clone 490063 5' (1110);	r .	٠.
		/note="DDS similarity to AA047548 zf15e02.rl Soares fetal heart NDH19W Homo sapiens cDNA clone 377018 5' (1. 138); 96% identityOther overlapping matches:-(1043510548) DDS similarity to AA136115 xk90h04 rl Soares program.		
		/rpt_family="Alu" 1040910548	misc_feature	
misc_feature		frame: 1, quality: excellent, score: 75.000" complement(992810123)	repeat_region	
repeat_region		ITAME: 1, quality: good, score: 63.000"  complement(96299672)  note="predicted exon program: gradilocope human 1 3	misc_feature	
		<pre>complement(94459505) /note="predicted exon, program: grail2exons_human_1.3,</pre>	misc_feature	
		9358 9535 /rpt_family="LTR12"	repeat_region	
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		emen famí	repeat_region	
misc_feature		<pre>complement(64866772) /rpt_family="Alu"</pre>	repeat_region	
repeat_region	·	54255722 /rpt_family="Alu"	repeat_region	
repeat_region		/rpt_family="Alu"	rebear_redion	
٠.		/standard_name="endogenous retroviral sequence" /note="HERV9 retroviral sequence"		
		reale: 1, quarity: good, score: 62.000" 22578516	LTR	
		edicted e		
		/ "UVET PIEUTCEE EACH, PIOSIAM: 914112EXCHS_HUMBH_1.3, frame: 1, quality: good, scoré: 71.000"	misc feature	
		640)	misc_feature	
misc_feature		complement(662)	repeat_region	
repeat_region		flow-sorted chromosomes from hybrid 5HL2-B, which carries chromosome 19 as its only human chromosome."		
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		/chromosome="19"		
		/organism="Homo sapiens" /db_xref="taxon:9606"	·	
		1. 40668	source	
		11 Laboratory, 7000 East Ave., Livermore, CA 94551, USA Location/Oualifiers		
		-NOV-1997) Himan Genome Center Lawrence		
misc_feature		2 (bases 1 to 40668)	JOURNAL Unpublished REFERENCE 2 (bases 1	<u>.</u> .
		e analysis of an ~1 Mb region containing the MEF2B gene in		
		Garnes, J., Danganan, L., Bruce, R., Quan, G., Montgomery, M., Ow, D., Kobayashi, A., Olsen, A.O. and Carrano, A.V.	Garne Kobay	
		aryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; heria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 40668)	Eukaryota; Eutheria; REFERENCE 1 (bases	
-			ORGANISM Homo s	
misc_feature		39 12.1 GI:2636669	S	
		te, complete sequence.	ACCESSION AC003112	
		•	LOCUS AC003112 DEFINITION Human DNA	

. .14885) DDS similarity to AA121532

terus NbHPU Homo sapiens cDNA 9% identity.~~(15227. .14885)

/note-PDDS similarity to AA136115 zk90b04.rl Soares /note-PDDS similarity to AA136115 zk90b04.rl Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490063 5' (193. .394); 94% identity.--DDS similarity to AA009412 ze82h02.rl Soares fetal heart NbH19W Homo sapiens cDNA clone 365523 5' (145. .346); 96% identity.--(11121. .11331) DDS similarity to AA009693 ze82h02.sl Soares fetal heart NbH19W Homo sapiens cDNA clone 365523 3' (429. .307); 95% identity.--(11127. .11246) DDS similarity to AA047548 zf15e02.rl Soares fetal heart NbH19W Homo sapiens cDNA clone 377018 5' (222. .341); 97% identity.--(11061. .11331) /note-"predicted exon, program: grail2exons\_human\_1.3, frame: 1, quality: excellent, score: 100.000-DDS similarity to AA047548 zff.5e02.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone 377018 5' (139. .221); 100% identity.--DDS similarity to AA136115 zk90b04.rl Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490063 5' (111. .192); 99% identity.--DDS similarity to AA435628 identity.~~(13756. .13984) DDS similarity to AA450010 zx33f04.sl Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 788287 3' (228. 1); 99% identity.~" complement(13274. .13531) /rpt\_family="Alu" total fetus Nb2HF8 9w Homo sapiens (309. 229); 99% identity.~" complement(12966. 13240) /rpt\_family="Alu" /note="predicted exon, program: grail2exons\_human\_1.3, frame: 2, quality: good, score: 61.000--Other overlapping matches:-(13756..13826) DDS similarity to AA009412 ze82h02.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone 365523 5' (428..496); 97% identity.--(13756..13984) DDS similarity to AA009693 ze82h02.sl Soares fetal heart NbHH19W Homo sapiens cDNA clone 365523 3' (227..1); 98% complement(11869. .12161)
/rpt\_family="Alu" predicted exon, program: grail2exons\_human\_
quality: good, score: 73.000--(11061. .1120
similarity to AA452628 zx33f04.r1 Soares to zx33704.rl Soares total fetus ND2HF8 9w Homo sapiens cDNA clone 788287 5' (83. 165); 100% identity.--DDS similarity to AA009412 ze82h02.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone 365523 5' (62. .144); 100% identity." clone 788287 5' (1. .82); 95% identity.--(10486. .10548 similarity to AA009412 ze82h02.r1 Soares fetal heart NDHH19W Homo sapiens cDNA clone 365523 5' (1. .61); 97% 'note-"DDS similarity to AA136115 zk90b04.rl Soares 'note-"DDS similarity to AA136115 zk90b04.rl Soares 'regnant uterus NbHPU Homo sapiens cDNA clone 490063 5' (395. 477); 92% identity, --DDS similarity to AA009412 (282h02.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone 365523 5' (347. 427); 94% identity, --DDS similarity to AA009693 ze82h02.si Soares fetal heart NbHH19W Homo sapiens cDNA clone 365523 3' (306. 228); 99% identity, --DDS similarity to AA450010 zx33f04.sl Soares identity, --DDS similarity to AA450010 zx33f04.sl Soares LEMILARILY TO AA452628 zx33f04.rl Soares total fetus D2HF8 9w Homo sapiens cDNA clone 788287 5′ (167. .313); 18% identity " identity 10725 Soares total fetus Nb2HF8 .14029) DDS similarity to AA452628 9w Homo sapiens cDNA y.~~(10486. .10548) frame: 0, 307); 95% .11331) DDS

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Best Local Similarity 59.9
Matches 1862; Conservative
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//note="predicted exon, program: grail2exons_human_1:3,
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0; Mismatches 981;
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Similarity 99.6%;
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Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S.,
Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
Kikuchi,Y.
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NTSTLALALANINGSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPENISCWSRNMK
DLTCEWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPY
EIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKD
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/db_xref="GI:4774668"
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/db_xref="PID:e1433696"
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                                                                                                                                                                                                                                                                                                                                                                       243;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Elson, G.C.A., Graber, P., Losberger, P., Herren, S., Menoud, L.N., Wells, T.N.C., Kosco-Vilbois, M.H. and Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Elson,G.C.A., Graber,P., Losberger,P., Herren,S., Gretener,D., Menoud,L.N., Wells,T.N.C., Kosco-Vilbois,M.H. and Gauchat,J.F. CLF-1, a Novel Soluble Protein Shares Homology With Members of Cytokine Type-I Receptor Family
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/protein_id="AAC3835.1"
/protein_id="AAC3835.1"
/protein_id="AAC3835.1"
/db_xref="piD:9372627"
/db_xref="GI:3372627"
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/product="cytokine-like factor-l"
623 c 525 g 273 t
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RVEDSVDWKYYDDVSNQTSCRLAGLKPGTYYFYQVRCNPFGIYGSKKAGIWSEWSHPT
RASTPRSERPGPGGGACEPRGGEPSSGPYRRELKQFLGWLKKHAYCSNLSFRLYDQWR
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/map="19p12"
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/db_xref="taxon:9606"
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Pred. No. 1.5e-36;
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                                                                                                                                                                                                                                                                                                                                      8604 gtgaccacggacccccccccccgacgtgcacgtgagccgcgttgggggcctggaggaccag
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CTGAGCGTGCGCTGGGTGTCGCCACCCCGCCCTCAAGGATTTCCTCTTTCAAGCCAAATAC
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1 (bases 1 to 1391)

Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S., Zhang,J., Alexander,W:, Hilton,D.J., Kojima,T., Maeda,M. and
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/protein_1(="Cab42576.1"
/protein_1(="Cab42576.1"
/db_xref="piD:e1433703"
/db_xref="piD:e1433703"
/db_xref="piD:g4774673"
/db_xref="61:4774673"
/db_xref="61:4774673"
/db_xref="61:4774673"
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SCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRGGEPSSGPVRRELKQFLGWĽKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQHRTRGS
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/db_xref="taxon:32644"
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Pred. No. 2.5e-30;
D; Mismatches 37
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al Similarity 92.0%;
149; Conservative
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Genomic architecture and transcriptional activation of the mouse and human tumor susceptibility gene TSG101: common types of short transcripts are true alternative splice variants
                                                                                                                                                                             AF060868
g3776298
                                                                                                                                                                                                                    Mus musculus tumor
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A70393.1
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                                                                                                                                                                                                                                    AF060868
                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammal.
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 . (bases 1 to 33613)
Wagner, K.U., Dierisseau, P., Rucker, E.B. III, Robinson, G.W.
                                                                                                                   Mus musculus
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Nicola, N.A., Fabri, L., E
Zhang, J., Alexander, W.,
Kikuchi, Y.
                                               Hennighausen, L.
                                                                                                                                  house mouse
                                                                                                                                                                                                        complete cds
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/db_xref="taxon:32644"
182 c 165 g 100
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from Patent
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Pred. No. 7.9e-20;
0; Mismatches 13;
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WO9811225.
gene TSG101: common types of shorter re splice variants
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Best Local Similarity

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                                                                                                         AF139987 114898 bp DNA Mus musculus LIM-kinasei (Limki) gene,
                                              (Wbscr1) gene, alternative splice replication factor C, 40kDa subuni AF139987
house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (22-APR-1998) LGP, NIDDK, NIH, Bdg. 10, Rm. 9N115
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99054675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.18;
ilarity 76.48;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGTISEDTIRASLISAVSDKLRWRMKEEMDGAQAELNALKRTEEDLKKGHOKLEEMVT
RLDQEVAEVDKNIELLKKKDEELSSALEKMENQSENNDIDEVIIPTAPLYKQILNIYA
EENAIEDTIFYLGEALRRGVIDLDVFLKHVRLLSRKQFQLRALMQKARKTAGLSDLY"
1 6833 c 7411 g 10390 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NDGSSRELVNLTGTIPVRYRGNIYNIPICLWLLDTYPYNPPICFVKPTSSMTIKTGKH
VDANGKIYLPYLHDWKHPRSELLELIQINIVIFGEEPPVFSRPTVSASYPPYTATGPP
NTSYMPGMPSGISAYPSGYPPNPSGYPGCPYPPAGPYPATTSSQYPSQPPYTTYGPSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="tumor susceptibility protein 101"
/protein_id="AAC83576.1"
/db_xref="piD:g3776299"
/db_xref="GI:3776299"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MAVSESQLKKMMSK!KYRDLTVRQTVNVIAMYKDLKPVLDSYVF"/
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15529. .15655,19105. .19171,21556. .21647,30206. .30408
11594. .31833,33056. .33385)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="129/SvJ"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="tsg101"
                             GI:4972948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #4"-tumor susceptibility protein 101"
#44-.2885,9233. 9317,11875. 11940,13615.
.15655,19105. .19171,21556. .21647,30206.
.31833,33056. .33145)
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                                                                   usel (Limkl) gene, complete cds; wbscrl ative splice products, complete cds; and 40kDa subunit (Rfc2) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 132; DB 12;
Pred. No. 4.1e-18;
0; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 33613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                              polyA_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 of 114898)
1 (bases 1 of 114898)
Martindale, D.W., Wilson, M.D. and Koop, B.F.
Martindale, D.W., Wilson, M.D. and Koop, B.F.
Comparative genomic sequence analysis of the Williams syndrome
Comparative genomic sequence 7q11.23 containing the LIMKI, WBSCRI,
WBSCRI, Tank region in mouse chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Environmental Health, University Victoria, BC V8W 3N5, Canada Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (01-APR-1999) Department of Biology, Environmental Health, University of Victoria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
Eukaryota; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Rodentia; Sciurognathi; Murida
(bases 1 to 114898)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 114898)
Martindale,D.W., Wilso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MRLTLLCCTWREERMGEEGSELPVCASCGQRIYDGQYLQALNAD
WHADCFRCCECSVSLSHQYYEKDGQLFCKKDYWARYGESCHGCSEHITKGLYMVAGEL
KYHPECFICLACGNFIGDGDTYTLVEHSKLYCGQCYYQTVVTPVIEQILPDSPGSHLP
/translation="MADFDTYDDRAYSSFGGGRGSRGSAGGHGSRSQKELPTEPPYTA
YVGNLPFNTVQGDIDAIFKDLSIRSVRLVRDKDTDKFKGFCYVEFDEVDSLKEALTYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVGNPYWMAPEMINGRSYDEKVDVFSFGIVLCEIIGRVNADPDYLPRTMDFGLNVRGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPSDLIHGEVLGKGCFGQAIKVTHRETGEVMVMKELIRFDEETQRTFLKEVKVMRCLE
HPNVLKFIGVLYKDKRLNFITEYIKGGTLRGIIKNMDSQYPWSQRVSFAKDIASGMAY
                                                           /product="Wbscr1"
/protein_id="AAD34859.1"
/db_xref="PID:g4972950"
                                                                                                                                                                                                                                                             join(52154. .52241,6
66975. .67034,69389.
/gene="Wbscrl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDRYCPPNCPPSFFPITVRCCDLDPEKRPSFVKLEQWLETLRMHLSGHLPLGPQLEQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VHTPSGQAASSARQKPVLRSCSIDTSPGTSSLASPASQRKDLGRSESLRVVCRPHRIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="LIM-kinase1"
/protein_id="AAD34858.1"
/db_xref="PID:g4972949"
                                                                                                                                                                               gene="Wbscr1
oin(52183. .
                                                                                                                                                                                                                                                                                'product="Wbscr1 alternative spliced product",
join(52154. .52241,63700. .63887,65870. .65934,
56975. .67034,69389. .69526,69827. .71599)
                                                                                                                                                                                                                                                                                                                                                                                                           /gene-"Limkl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'db_xref="GI:4972949"
                                          db_xref="GI:4972950"
                                                                                                                                                                                                                                                                                                                                                  gene="Wbscr
                                                                                                                                                                                                                                        product-"Wbscr1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMNIIHRDLNSHNCLVRENRNVVVADFGLARLMIDEKNQSEDLRSLKKPDRKKRYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ene-"Limkl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               b_xref="taxon:10090"
lone="Genome Systems Inc BAC17511"
ln(2873. 3130,4731. 4827,18321. .18459,18691
ln(2873. 3130,4731. 4827,18321. .22557,25458
947. .21153,22176. .22281,22391. .22557,25458
178. .26264,27155. .27286,29309. .29368,29613
468. .31624,33507. .33562,33821. .33978,34086
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                                                                                                                                                                                                                                                                                                                                                                                        ln(52154.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n(3076
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                                                                                                                                                                                                                                                                                                                                                  2154. .52241,63700. .6
.69526,69827. .71599)
"Wbscrl"
                                                                                                                                                            2183 .52241,63700 .63887,65870 .65934,66013 .66109,
.67034,69389 .69526,69827 .69966)
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26264,27155. .27286,29309.
31624,33507. .33562,33821.
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ae; Murinae;
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Best Local S
Matches 174
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                                          gtgggccacca 4255
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                                                                                                                                                                                                  tttttgagacagggtttctctgtacagccctggctgccctggcactcattctgtagacca
                                                                                               GGCTGGCCTCAAACTCAGAAATCCGCCTGCCTGTGCCTCCCAAGTGCTGGGATTAAAGAT
                                                                                                                                                                               TTTTTGAGACAGGGTTTCTCTGTACAGCCCTGGCTGTCCTGGAACTCACTTTGTAGACCA
                                                                                                                                                                                                                                                                                                                                                                                                                            174;
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                43269
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Pred. No. 2.7e.

Mismatches

; 2.7e-17; 77;

Indels

0; Gaps

0

4184

43340

43280

Length 114898;

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/translation="MEVQESGCDPSESGAQEPSPVPSKTAGHYELPWVEKYRPLKLNE
IVGNEDTVSRLEVFAREGNVPNIIIAGPPGTGKTTSILCLARALLGPALKDAVLELNA
SNDRGIDVVRNKIKYEAQQKVTLPKGRHKIIILDEADSMTDGAQQALRETMEIYSKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="replication factor complement(93152. .103710)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSRFRDGPPLRGSNMDFREPTEEERAQRPRLQLKPRTVATPLNQVANPNSAIFGGARP
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DFLGGRGGSRPGDRRAGPPMGSRFRDGPPLRGSNMDFREPTEEERAQRPRLQLKPRTV
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                                                                                    | TAQGDMRQALNNLQSTFSGFGYINSENVFKVCDEPHPLLVKEMIQHCVDANIDEAYKI
                                                                                                                 RFALACNASDKIIEPIQSRCAVLRYTKLTDAQVLTRLMNVIEKEKVPYTDDGLEAIIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="Rfc2
                                                          AHLWHLGYSPEDVIGNIFRVCKTFPMAEYLKLEFIKEIGYTHMKVAEGVNSLLQMAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="Rfc2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene-"Wbscrl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="Wbscrl alternative
/protein id="AAD34860.1"
                                                                                                                                                                                                                          protein_id="AAD34861.1
db_xref="PID:g4972952"
db_xref="GI:4972952"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein_id="AAD34860.1
db_xref="PID:g4972951"
db_xref="GI:4972951"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pmplement(join(93152. .93630,94484. .94597,96116.
7205. .97270,98133. .98290,100260. .100360,100502.
D2020. .102126,102503. .102549,104514. .104583,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ltanslation-"madfdTyddrayssfgggrgsrgsagghgsrsqkelpteppyta
GNLPFNTVQGDIDAIfKDL3IRSVRLVRDKDTDKFKGFCYVEFDEVDSLKEALTYD
ALLGDRSLRVDIAEGRKQDK3GFGFRKGGPDDRGYRDDFLGGRGGSRPGDRRAGPPM
                                                                                                                                                                                                                                                                                              product="replication factor
protein id="AAD34861.1"
                                                                                                                                                                                                                                                                                                                                      :cdon_start=1
                                                                                                                                                                                                                                                                                                                                                                                              lement(join(93520. 93630,94484. 94597,96116. 5. 97270,98133. 98290,100260. 100360,100502. 20. 102166,102503. 102549,104514. 104583, 95. 108692))
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69526,69827. .69966)
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REFERENCE
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Ow, D., Nolan, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Burkhart-Schultz,K., Gordon,L., Kyle,A., Ramirez,M., S
Garnes,J., Danganan,L., Poundstone,P., Christensen,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burkhart-Schultz,K., Gordon,L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 157684)
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        /rpt_family="AT_rich"
complement(11272...11610)
/note="predicted exon, program: grame: 1, quality: good, score: 51
complement(12688...12820)
/rpt_family="FLAM_C"
complement(13313...13358)
/rpt_family="""
                                                                                                                                                                                                                                                                                                                   /note-"predicted exon, program: grail2exons_human_1.3, frame: 1, quality: good, score: 52.000" complement(5770. 6199)
/note-"BLASTN similarity to U17089 (72. .503); match: 0.93, score: 8.5e-139; database searched: nt; Mus musculus MT transposon-like element, clone MT17."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="BAC-10817"
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                                                                                                                                                                                    plement(9833...,9908)
te="predicted exon, program: grail2exons_human_1.3,
me: 2, quality: excellent, score: 86.000"
50, 10173
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"e="BAC clone obtained frrom Genome Systems."

from cell line CJ7, derived from mouse stra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family-"(GGA)n"
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="predicted exon,"
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family="POLY_A"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 predicted exon, program: grail2exons_human_1.3,
0, quality: excellent, score: 86.000*
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   T_rich".
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                                                                              grail2exons_human_1.3,
51.000"
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                                                                                             'Tpt_family="(CA)n"
77440. 27585
'note="Low confidence in sequence within low complexity
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rame: 2, quality: good,
                                                                                                                                                                                                            __family="7SLRNA"
lement(25390, .25465)
_familv="""
                                                                                                                                                                                        family="Alusp"
7. .25637
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t_family="(TAAAA)n"
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t_family="AT_rich"
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lement(253==
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32881|sp|P12947|RL31_HUMAN 60S RIBOSOMAL PROTEIN L31;
1328|pir||R5HU31 ribosomal protein L31 - human;
1329|pir||R5RU31 ribosomal protein L31 - rat; gi|36130
                                                                                                                                                                      family-"AluSq/x"
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1. .24798
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3. .23867
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lement(15549. .15632)
_family="AluJo"
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i, quality: good, score: 67.000"
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16419
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t(16233
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d, score:
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gi|1632855|gnl|PID|e276436
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52.000"
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              | teattotgtagaccaggetagceteaaactcacaaacctacctgcctctgcctttccagt 4229
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TCACTTTGTAGACCAGGCTGGCCTCAAACTCAGAAATCCACCTGCCTCTGCCTCCCGAGT 154764
                                                   GITGITGITGITGITITTCGAGACAGGGITTCTCTGTATAGCCCTGGCTGTCCTGGAAC 154824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="AT_rich"
complement(37247. 37346)
/rpt_family="(GAA)n"
complement(37348. 37505)
/rpt_family="FRAM"
                                                                                                                                                                                                                                              44327
                                                                                                                                                                                                                                                                                                                                                            rame: 2, quality: good, score: complement(41066. .41217)
/rpt_family="FRAM"
11459. .41070
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/rpt_family="AluJ/monomer"
complement(43492. .43523)
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complement(33730. .33788)
/rpt_family="L1MB8"
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/rpt_family="AT_rich"
complement(30815..30844)
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/rpt_family="L1"
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/rpt_family="AT_r:
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3. .34850
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ement(3/)
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Pred. No. 2.9e
0; Mismatches
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72.000"
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65,000"
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74.000"
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66.000"
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TCTTTT 154698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burkhart Schultz, K., Gordon, L., Kyle, A., Ramirez, M., Stilwagen, S., Phan, H., Velasco, N., Garnes, J., Danganan, L., Poundstone, P., Christensen, M., Georgescu, A., Andro, L., Liu, S., Antix, C., Andreise, T., Trankheim, M., Amico-Keller, G., Coefield, J., Duarte, Lucas, S., Bruce, R., Thomas, P., Quan, G., Kronmiller, B., Arellano, Montgomery, M., Ow, D., Nolan, M., Trong, S., Kobayashi, A., Olsen, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Carrano, A.V.
Sequence analysis of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 128026)
Lamerdin, J.E., McCready, P.M., Skowronski, E., Adamson, A.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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                                                                                                                                                                                                                                /rpt_family="AT_rich
complement(1415. .15
                                                                                                                                                                                                                                                             frame: 1, quality: gcod, complement(712. .742)

/rot family="aff rich"
                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="(CAAAA)n"
complement(489...532)
/rpt_family="(CCAA)n"
complement(544;..596)
                                                                               complement(3882..39
/rpt_family="(CAA)n"
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rpt_family="(GGGA)n"
                                                                                                                    rpt_family="(CA)n"
                                                                                                                                                                                                                                                                                                                                        'rpt_family="Alus"
29. .661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'lab_host="HS996 (modified DH10B/r)"
'note="Clone 10818 containing mouse Ercc-4 obtained epome Systems. CJ7 cell line is derived from mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
ob_xref="taxon:10090"
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                                     _family="(GAAAA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             line="CJ7"
                                                                                                                                                                                                                                                                                                                  predicted exon,
                                                                                                                                                                     y-"AluJ/FLAM"
                                                                                                                                                                                                          y="(CA)n"
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                                                                                                                                                                                                                                                                                                program:
d, score:
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Livermore,
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66.000"
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Olsen, A.O.
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frame: 2, quality: excellent, scol
complement(13670. 13799)
/rpt_family="MERS58A"
complement(13821. 14009)
/rpt_family="(CA)n"
                                                                                                                                                                complement(21689 .21837)
note="predicted exon, program:
frame: 1, quality: good, score:
22204 22364
                     rpt_family="(GGGA)n"
                                                                                                       note="predicted exon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               frame: 1, quality: good,
complement(9566. .9669)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"predicted exon, program: grail2exons_mouse_1.3, frame: 0, quality: good, score: 56.000" complement(6066. .6114) /rpt_family-"(GA)n" complement(6114. .6222) /rpt_family-"(CA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(5418. .5622)
/rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(5696
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pt_family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                        _family="AT_rich"
lement(19060, 19010, family=""
                                                           _family=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _family-"AluJo/FRAM"
lement(16003, .16110, family-"/-
                                                                                                                                                                                                                     family="(CA)n"
                                                                                                                                                                                                                                                                                                                                    family-"L1MC3"
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ement(17195. .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  family="LINE2"
                                                                                                                                                                                                                                                                                nent(20409. .20528)
predicted exon, program:
0, quality: good, score:

, cuality: excellent, score: 87.000
23579

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1, quality: good, score: 53.000"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                predicted exon, program: grail2exons_mouse_1.3,
quality: good, score: 51.000*
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19219)
19257
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181
                                                                                                                                                                                                                                                   -"(GGAA)n"
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                                                       "(GAAAA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "(GGA)n"
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                                                                                                                                                                   grail2exons_mouse_1.3,
53.000"
                                                                                                                                                                                                                                                                                 grail2exons_mouse_1.3, 65.000"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          grail2exons_mouse_1.3,
core: 83.000"
                            Š
                                                       Query Match 1.1%;
Best Local Similarity 74.8%;
Matches 160; Conservative
                                                                             Query Match
Best Local
misc_feature
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/rpt_family="(GA)n" complement(37079
                                                                                                   complement(37079: .37151)
/note="predicted exon, program: grail2exons_mouse_1.3,
/rame: 1, quality: excellent, score: 100.000"
complement(37340: .37416)
/note="predicted exon, program: grail2exons_mouse_1.3,
/rame: 2, quality: good, score: 65.000"
                                                                                                                                                                                                                                                                                                                                    /note="BLASTX similarity to p21414 (545. .600); match: 0.73, score: 2.3e-178; database searched: nr; POL POLYPROTEIN (PROTEASE, REVERSE TRANSCRIPTASE complement(36157. .36532)
                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"BLASTX similarity to P21414 (709. .727); match: 0.73, score: 2.3e-178; database searched: nr; POL POLYPROTEIN (PROTEASE, REVERSE TRANSCRIPTASE" complement(35765. .35979)
                                                                                                                                                                                                                                                                                                      /rpt_family="HERVE"
/omplement/off/f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="AT_rich"
complement(25863. .25937)
/rpt_family="-"-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="MLT1E"
complement(25789. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="(GA)n"
23842. .24064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 omplement(35279. .35563)
ote-"BLASTX similarity to P21414 (817. .911); match: (
core: 2.3e-1/18; database searched: nr; POL POLYPROTEIN
ROTEASE , REVERSE TRANSCRIPTASE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pt_family="Alusp"
mplement(27004. .27134.
pt_family="""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pt_family="AluJo/FRAM"
uplement(30337, 3026)
t_famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _family="HERVR"
lement/2577
                                                                                                                                                                                                                                                                                                                                                                                                                  _family-"HERVHC;
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5. 32503)
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7. .28083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ly="(CATA)n"
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                                                       0
                                                      Score 127.6; DB 12;
Pred. No. 3e-17;
0; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "tRNA-Cys-TGC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "POLY_A"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CA)n"
                                                                                                                                                                                                                                                                                                                                                                                                   36156)
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pllent:, score: 76.000"
                                                                                 Length 128026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .911); match: 0.5,
                                                    0;
                                                  Gaps
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## GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 19, 1999, 11:40:06; Search time 244.65 Seconds (without alignments) 12100.032 Million cell updates/sec

Title: Perfect score:

Scoring table: IDENTITY\_NUC

Searched: 311585 seqs, 125096042 residues

N\_Geneseq\_36:\*

Database :

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result

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Query Match 100.0%; Score 11830.4; Best Local Similarity 100.0%; Pred. No. 0; Matches 11831; Conservative 0; Mismatches

DB 1; Length 11832; Indels

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New isolated haemopoietin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells

Claim 8; Page 108-114; 182pp; English.

The NR6 gene encodes a novel Haemopoietin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's products can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in
                                                                                                                                                          WO9811225-A2.

19-MAR-1998.

11-SEP-1997; G02479.

11-SEP-1996; AU-002246.

(AMRA-) AMRAD OPERATIONS PTY LTD.

(AMRA-) AMRAD OPERATIONS PTY LTD.

(AZIE/) DZIEGLEWSKA H E.

Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,

KOjima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
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CDS
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WPI;
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1301

CAGTGGCGTGCTTGGATGCAGAAGTCACACAAGACCCGAAACCAGGTAGGAAAGTTGGGG cagtggcgtgcttggatgcagaagtcacacaagacccgaaaccaggtaggaaagttgggg

1360

ttcctcggctggctcaagaagcacgcatactgctcgaaccttagtttccgcctgtacgac

11162

1240

11102

9t9t9cca9ccgcggggcggagccca9ctcgggcccggtgcggcgcgagctcaagcag

 Query Match Best Local S Matches 777

Local Similarity 96.

96.2%;

Score 737.2; DB 1; Pred. No. 1.7e-162; 0; Mismatches 28;

Indels Length

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Gaps

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11-SEP-1997; G02479.

11-SEP-1996; AU-002246.

4 (1M-SEP-1996; AU-002246.

A (AMRA-) AMRAD OPERATIONS PTY LTD.

A (DZIE/) DZIEGLEWSKA H E.

A (DZIE/) DZIEGLEWSKA H E.

7 Alexander W, Fabri L, Farley A, Hilton DJ

7 Aima T, Maeda M, Nash A, Nicola NA, Ray
                                                                                                                                                                                                                                                                                                                                                                                           V27118;
29-5EP-1998 (first entry)
29-5EP-1998 (first entry)
Unspliced murine NR6 nucleotide sequence.
Haemopoletin receptor; cell proliferation; cell differentiation;
annual; therapeutic; neuronal proliferation; drug screening survival;
Example 8; Page 99-100; 182pp; English.

NR6 is a novel haemopoletin receptor (HR). Interaction between the nov HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for Grug screening.

Sequence 1930 BP; 375 A; 623 C; 561 G; 371 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6612
                                                                                                                                                                                       WPI; 98-260970/23.
WPI isolated haemopoletin recommodulating proliferation, e.g. neuronal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V27158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1930
                                                                                                                                                                                                    receptor - used for lon, differentiation
                                                                                                                                                                                                                                                                       Rakar S, Willson
                                                                                                                                                                                                      developing products and survival of cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                      screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6663
                                                                                                                                     n the novel survival.
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W09811225-A2.

) 19-MAR-1998.

F 11-SEP-1997; G02479.

/R 11-SEP-1996; AU-002246.

/A (AMRA-) AMRAD OPERATIONS PTY LTD.

PA (DZIE/) DZIEGLEWSKA H E.

PA (DZIE/) DZIEGLEWSKA H E.

Alexander W, Fabri L, Farley A, Hilton DJ

""" Alexander W, Rab' A, Nicola NA, Ra)
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Zhang J;
WPI; 98.260970/23.

P-PSDB; W55013.

New isolated haemopoletin receptor - used for developing profor modulating proliferation, differentiation and survival o e.g. neuronal cells

Claim 6; Page 90-92; 182pp; English.

The haemopoletin receptor (HR) NR6.3 is a form of the novel Interaction between the novel HR and a ligand facilitates proliferentiation and survival of a wide variety of cells. The
                                                                                                                                                                                                   29-SEP-1998 (first entry)
Novel haemopoletin receptor NR6.3 gene.
Haemopoletin receptor; cell proliferation; cell survival; therapeutic; neuronal prolif Mouse.
Mus sp.
Location/Qualifiers
CDS
Location/Qualifiers
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V27142;
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                                                                                                                                                                                                                                                                                        DNA;
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                                                                                                                                                                                                                                     ntion; cell differentiation; cancer;
proliferation; drug screening; ss;
                                                                                                  n DJ, I
Rakar
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                                                                                                 Kikuchi Y,
r S, Willson
                                                  developing products and survival of cells,
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s proliferation,
The HR and it's
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                                                                                    acca--gaggctgggcacaatgagctcccacaaccaccagctttggtccacatgatggtca
                                                                                                                              gacctggaggctcacctgaattggagcccctctgtacc-atctgggcaacaaagaaacct
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Best Local Similarity
Matches 281; Conserv
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11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS PTY LTD.
(DZIE/) DZIEGLEWSKA H E.
(DZIE/) DZIEGLEWSKA H E.
N1-exander W, Fabri L, Farley A, Hilt
Mouse.
Mus sp
                               v27141 standard; cDNA; 1673
v27141;
29-SEP-1998 (first entry)
Novel haemopoletin receptor
Haemopoletin receptor; cell
                       cell survival;
                                                                                                                                                                           6570
                                                                                                                                                                                                                           6510
                                                                                                                                                                                                                                                                                                                              6390
                                                                                                                                                                                                                                                                                                                                                                               6330
                                                                                                                                                                                                                                                                                                                                                                                                                                                               The haemopoletin receptor (HR) NR6.1 is a form of the novel HR NR6. Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vitro. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening. Sequence 1629 BP; 336 A; 541 C; 453 G; 299 T;
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29-SEP-1998
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Key
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im 4; Page 77-81; 182pp;
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                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                         receptor; cell
l; therapeutic;
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/product= "Haemopoietin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor - used for ion, differentiation
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1 proliferation;
; neuronal prolif
                  NR6.2 gene. proliferation; cell difineuronal proliferation;
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bla NA, F
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5.9e-56;
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                     differentiation;
on; drug screeni
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              differentiation;
ion; drug screening
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Best Local Similarity
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WO9831811-A1.
23-JUL-1998.
15-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 84-87; 182pp; English.

The haemopoletin receptor (HR) NR5.2 is a form of the novel HR NR5.

Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.

Sequence 1673 BP; 344 A; 550 C; 474 G; 305 T;
                                                                                            26-OCT-1998 (first entry)
Nucleotide sequence of the murine U4
Murine; U4 protein; haematopoietin re
cell proliferation; immune response;
autoimmune disease; cancer; allergy;
                                                                                                                                                                                                                                                              6570
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New isolated haemopoletin reconstruction modulating proliferation, e.g. neuronal cells

Claim 5; Page 84-87; 182pp; E.
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                                                                                                                                                              V41688;
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19-MAR-1998.
11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
                                                                                                                                                                                                                                      489
                                                                                                                                                                                                                                                                                      429
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                                                                                                                                                                                                                                                                                                                                                                                                                                       249
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                                                                                                                                                                                                                                     GAGACGGCAGCATTCTGGCTGGCTCCTGCCTCTATGTTGGCT
                                                                                                                                                                                                                                                                                              ccctggctaaccttaatgggtccaggcagtcaggagacaatctggtgtgtcacgccc
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                                                          Location/Qualifiers 122. .1399
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Farley
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Nicola NA, Rakar S, Willson
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Pred.
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e; antibody;
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No. 7e-56;
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                                                                                                           differentiation;
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al of cells,
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This is the nucleotide sequence encoding the murine U4 protein from the haematopoietin receptor superfamily, used in the method of the invention for the modulation of cell proliferation, or the immune cresponse. Transformed mammalian cells are used to produce recombinant U4 protein is used to screen for specific binding agents, raise antibodies. It is also used as reagents for assays and capents, raise antibodies. It is also used as reagents for assays and stissue markers for isolation of cognate ligands and receptors, and coll differentiation, and the immune system (e.g. for treating immune cell deficiency, inherited or the result of infection, autoimmune diseases, cancer, and allergy).

So Sequence 1656 BP; 318 A; 552 C; 478 G; 308 T;
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Best Local Similarity 98.9%;
Matches 279; Conservative
Zhang J;
WPI; 98-260970/23.
D-PSDB; W55014.
                                                                               WO9811225-A2.
19-MAR-1998: G02479.
11-SEP-1997: G02479.
11-SEP-1996: AU-002246.
(AMRA-) AMRAD OPERATIONS P.
(DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Fari.
KOjima T, Maeda M, Nash A,
                                                                                                                                                                                                                                                                                                                                                                                                                  29-SEP-1998 (first entry)
Nucleotide sequence of products generated by SN race of brain cDNA.
Haemopoietin receptor; cell proliferation; cell differentiation; call survival; therapeutic; neuronal proliferation; drug screening;
                                                                                                                                                                                                                                                                                                                                          Mouse.
Mus sp
Key
CDS
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(GEMY) GENETICS INST INC
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L, Farley A, Hilton
Nash A, Nicola NA, 1
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Pred. No. 3.9e-55;
0; Mismatches 3;
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Best Local Sir
Matches 255;
                                                                                                                             01-MAY-1998; U08865.
13-FEB-1998; US-074721.
01-MAY-1997; US-045287.
01-MAY-1997; US-850030.
13-FEB-1998; US-023890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The nucleotide sequence was generated by a 5N RACE of brain cDNA using NR6 specific primers. NR6 is a novel Haemopoietin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening. Sequence 834 BP; 167 A; 274 C; 225 G; 168 T;
                        New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g. down-regulating Zcytor5 natural ligands or detecting cardiotrophin-liplood
                                                                           (ZYMO) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert
Lok S, Presnell SR, Whitmore
WPI: 99-034662/03.
                                                                                                                                                                                                                                                                                                cDNA encoding rat zcytor5.
zcytor5; cytokinin-like receptor; down-regulation;
maintenance factor; thyroid; heart; skeletal muscl
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Claim 7; Page 93-95; 182pp;
                                                                  P-PSDB; W70862.
                                                                                                                                                                                              WO9849307-A1.
                                                                                                                                                                                                                                                                                     cardiac pathology; heart enlargement;
                                                                                                                                                                                                                                                                                                                                                                  V70896 standard;
 The present
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55; Conservative
Page 72-75; 55pp; English sequence encodes a protein
                                                                                                                                                                                                                                                                                                                                          (first entry)
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/product= Zcytor5
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Pred. No. 5.9e-50;
0; Mismatches 1;
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protein
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and survival of cells
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                                                                                                                                                                                                                                                                                                            growth
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Best Local Sin
Matches 260;
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05-NOV-1998.
01-MAY-1998; U08865.
13-FEB-1998; US-074721.
01-MAY-1997; US-045287.
01-MAY-1997; US-850030.
13-FEB-1998; US-023890.
                                                                                                                                                                                                                                                                                                                                                                                                      V70894 standard;
V70894;
17-MAR-1999 (fir
        Disclosure; Page 63-66; 55pp; English.

The present sequence encodes a protein designated Zcytor5, which a cytokinin-like receptor. Soluble Zcytor5 may be administered town-regulate the effects of a growth and/or maintenance factor thyroid, heart, and skeletal muscle for example to lessen the effects.
                                                                                                                                                                                                                                                                                                                                               cDNA encoding human Zcytor5.
cDNA encoding human Zcytor5.
Zcytor5; cytokinin-like receptor; down-regulation; gromaintenance factor; thyroid; heart; skeletal muscle; cmaintenance factor; thyroid; heart; Zcytor5 ligand;
                                                                                New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g. down-regulating Zcytor5 natural ligands or detecting cardiotrophin-lin blood
                                                                                                                                             (ZYMO) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert
Lok S, Presnell SR, Whitmore
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sequence 1724 BP; 350 A; 550 C; 500 G; 324 T;
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Pred. No. 2.6e
0; Mismatches
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                                      Zcytor5, which administered to
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e; cardiotrophin-1;
nd; ss.
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05-NOV-1998.
01-MAY-1998; U08865.
13-FEB-1998; US-074721.
01-MAY-1997; US-045287.
01-MAY-1997; US-050309.
Disclosure: Page 68-70: 55pp; English.

The present sequence encodes an allelic variant of protein designated Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence
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cDNA encoding an allelic varaint of human
%cytor5; cytokinin-like receptor; down-reg
maintenance factor; thyroid; heart; skelet
                                                                                                                                             New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g. down-regulating Zcytor5 natural ligands or detecting cardiotrophin-1
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Adams RL, Foster
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                                                                                                                                                                                          2) ZYMOGENETICS INC.

S RL, Foster DC, Gilbert

S, Presnell SR, Whitmore

99-034662/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                pathology; heart enlargement;
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Pred. No. 3.4e
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t; skeletal muscle; cardiotro
ent; Zcytor5 ligand; allelic
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Best Local Sir
Matches 244;
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23-JUL-1998
15-JAN-1998; U00334
16-JAN-1997; US-784863
(GEMY) GENETICS INST IN
COllins M, Donaldson DD,
WPI; 98-414109/35.
                                                                                                                                       New nucleic acid encoding U4 haematopoletin receptor superfamily chain - potentially useful, e.g. for modulating cell proliferation or immune response, for treating cancer and auto:immune disease Claim 1; Page 28; 38pp; English.

This is the nucleotide sequence encoding the human U4 protein from the haematopoletin receptor superfamily, used in the method of the invention for the modulation of cell proliferation, or the immune response. Transformed mammalian cells are used to produce recombinant U4 protein. The U4 protein is used to screen for specific binding agents, raise antibodies. It is also used as reagents for assays and as tissue markers for isolation of cognate ligands and receptors, and the protein of cognate ligands and receptors, and
in pharmaceutical compositions which may modulate cell prolifer cell differentiation, and the immune system (e.g. for treating deficiency, inherited or the result of infection, autoimmune dicancer, and allergy).

Sequence 1579 BP; 304 A; 535 C; 473 G; 267 T;
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Nucleotide sequence of the human U4 gene.
Human; U4 protein; haematopoietin receptor superfamily;
cell proliferation; immune response; antibody; cell dif
autoimmune disease; cancer; allergy; ds.
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V41689;
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Pred. No. 3.
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hes 37;
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                                                                                                                 proliferation,
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Query Match Best Local Similarity

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Query Match Best Local S Matches 291

1.6%; Similarity 73.5%;

Conservative

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Score 190.8; Pred: No. 5.3e 0; Mismatches

.3e-35;

Indels

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Gaps

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RESULT 13
V27144
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AC V27144
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                          P-PSDB; W55015:

New isolated haemopoletin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells

e.g. neuronal cells

Claim 7; Page 102-104; 182pp; English.

The NR6 gene encodes a novel Haemopoletin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequence of clone HFK-66 encoding Haemopoietin receptor; cell proliferation; cell survival; therapeutic; neuronal prolifer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9811225-A2.
19-MAR-1998.
11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
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        1391 BP;
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  predisposition to
281 A; 459
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  to cancers,
59 C; 417
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     for drug screening.
234 T;
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                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                    Disclosure; Page 101; 182pp; English.

NR6 is a novel haemopoletin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for vitro and in vivo. They can be present and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.

Sequence 560 BP; 113 A; 182 C; 165 G; 100 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alexander W. Fabri
Kojima T. Maeda M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
W09811225-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated haemopoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell survival;
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                                                                                                                                                                                                                                                                                                                                                                                            for modulating proliferation, e.g. neuronal cells
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(DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
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11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
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                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for human NR6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor; cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        therapeutic;
                                                                                                                                                                1.2%; 92.0%;
                                                                                                                                                                                                                                                                                                                                                                                                       receptor - used for developing products ion, differentiation and survival of cells,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proliferation; cell difi
neuronal proliferation;
                                                                                                                                                                Score 141.2; DB 1
Pred. No. 1.3e-23;
                                                                                                                                                 Mismatches
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VERSITATION OF THE PRINCIPLE PRINCIP
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ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.

Sequence 143 BP; 42 A; 30 C; 50 G; 21 T;
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Key
CDS
                                                                                                                                                                                                                                                                                                                                                                New isolated haemopoletin receptor - used for developing products for modulating proliferation, differentiation and survival of cells e.g. neuronal cells
Disclosure: Page 98; 182pp: English.
The nucleotide sequence is unique to brain NR6. NR6 is a novel haemopoletin receptor (HR). Interaction between the novel HR and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence unique to 5N RACE of brain cDNA. Haemopoletin receptor; cell proliferation; cell differentiation; cell survival; therapeutic; neuronal proliferation; drug screeni
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS
(DZIE/) DZIEGLEWKA H E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9811225-A2.
19-MAR-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    502 CAGATCCGCTACCGAGTGGAGGACAGTGTGGAATGGAAGGTG
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/note= "No stop codon given"
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sh A, Nicola NA, I
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Rakar S, Willson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       developing products
and survival of cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       543
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ACAGCT
                        actgct 456
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                                                                        gcaactttcaaactctctggggaaggaaggaggctgaaaggggttgaacggggttcaggt 450
                                                                                                                GGCATGAAGGCTTAGGGTGGGGGATCGGTAGGACCCATGCACCCAGAGAAAGGGACTGGTG
                                                                                                                                                                            123;
                                                                                                                                                                                        Similarity
                                                                                                                                                                          Conservative
                                                                                                                                                                                       1.0%;
                                                                                                                                                                         0
                                                                                                                                                                         Score 121.2;
Pred. No. 3.36
0; Mismatches
                                                                                                                                                                    3.3e-19;
3;
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Best Loc Matches Query Match

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Search Job tir

completed: September 19,
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REFERENCE/DOCKET NUMBER:

NUMBER:

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Best Local Similarity 78.4
Matches 131; Conservative
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                                                                                                                                             CLASSIFICATION: PRIOR APPLICATION DATA:
                 TELEPHONE: 212 790-9090
                                                                                          APPLICATION NUMBER: 07/7
FILING DATE: 10-SEP-1991
TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                               URRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
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               ELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCTCTGGCTGTCC-TGGAACTCACTTTATAGACCAAGCTGGCCTCGAACTCAGAAATCC 1237
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                                                                                                                                                                                                                                                                                                                      10036-2711
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                                                                                                                                                                                                                                                                                                                                                                     New York
                                                                                                                                                                                                                                                                                                                                                                                                                                              INVENTION: Human And Murine Interleukin-5 Receptor
                                                                                                                                                                                                                                                                                                                                                 New York
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                                                                                                                                                                                                                                                                                                                                                                                 1155 Avenue of the Americas
212 8698864/9741
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                                                                                                                                                                                                                             PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takagi, Satoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tominaga, Akira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takatsu, Kiyoshi
                                                                                                                                                                                                                                                                                                                                                                                                    Pennie & Edmonds
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                                                                                S. Lesl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.8%;
                                                                                                                             07/757,390
                                                                                                                                                                                               US/08/442,281
                                                           18,872
                                               7005-030
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                                                                                                                                                                                                                              Version #1.25
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; LOCATION:
US-08-442-281-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL
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                                                                                                                                       NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: DORNER, F. APPLICANT: SCHEIFLINGER.
                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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                                                                                               ELECOMMUNICATION INFORMATION:
                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                       APPLICATION NUMBER:
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TOPOLOGY: 11r
                                                                 ELEFAX:
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                                                                                                                                                                           CATION NUMBER: EP 91 114 300.6
NG DATE: 26-AUG-1991
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                                                                (703)683-4109
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                                                                                                              30472/114 IMMU
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Pred. No. 6.7e-15;
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                                                                                                                                                                                                                                                                                                                    Version #1.25
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1355 base pairs
TYPE: nucleic acid
GTENNERUESE
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Best Local Similarity
Matches 131; Conserv
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                                                                                                                 COMPUTER READABLE FORM:
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APPLICATION NUMBER: 07/7:
FILING DATE: 10-SEP-1991
ATTORNEY/AGENT INFORMATION:
                   SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                  ORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                   COMPUTER: IBM PC
OPERATING SYSTEM:
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                                                                                               MEDIUM TYPE:
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                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                    OUNTRY: U.S.A.
IP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gcctgcttgtgcttcccaagtgcttagattaaaggtgtgcactgcca 5699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agtcctggctgtccttggaactcactctgtagaccaggctggccttgaactcagaaatcc 5652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCTCTGGCTGTCC-TGGAACTCACTTTATAGACCAAGCTGGCCTCGAACTCAGAAATCC 1237
                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                                                                                                                                                                            New York
                                                                                                                                                                                                                                                                                     T: Tominaga, Akira
T: Takagi, Satoshi
T: Murata, Yoshiyuki
INVENTION: Human And Murine Interleukin-5 Receptor
                                                                                                                                                                      New York
                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08442282
                                                                                                                                                                                                              1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                 Takatsu, Kiyoshi
                                                         IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                  Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
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US/08/442,282
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Pred. No. 6.7e-15;
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Best Local Similarity 78.4
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                tent No.
                CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5653 gcctgcttgtgcttcccaagtgcttagattaaaggtgtgcactgcca 5699
                                                                                       CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Takatsu, Kiyoshi
APPLICANT: Tominaga, Akira
APPLICANT: Takagi, Satoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                          STATE: New York
                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
APPLICATION NUMBER:
                                                                      APPLICATION NUMBER:
                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                 LICANT: Murata, Yoshiyuki
LE OF INVENTION: Himm
BER OF SECTION:
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    Application US/08442281
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78.4%;
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07/757,390
                                                                      US/08/442,281
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                                                                                                       Version #1.25
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US-07-757-390-16/c
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Best Local Similarity
                                                                                                                               Sequence 16, Application US/07757390
                                                                                                             Patent No.
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                                                                                                                                                                                                                                                                                                                                                                    1355 GTGTTCATTTTTGTTTGTTTGTTTGTTTGTTTTTTCGAGACAGGGTTTCTCTGTGT 1296
                                                                                                                                                                                                                                                                                                                                                                                           5533 gtttgtatttggttttggtttgagttttgttttatttgagacagggcttctctgtgtgt 5592
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Misrock, S. Leslie
Misrock, S. Leslie
76
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,390
FILING DATE: 19910910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 18, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                              AGCTCTGGCTGTCC-TGGAACTCACTTTATAGACCAAGCTGGCCTCGAACTCAGAAATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  131;
                                                                                            INFORMATION:
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Takagi, Satoshi
Murata, Yoshiyuki
                                    Tominaga, Akira
Takagi, Satoshi
                                                                           Takatsu, Kiyoshi
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And Murine Interleukin-5 Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 99; DB 1; Pred. No. 6.7e-15; 35;
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Best Local Similarity
                                                                                                                                                                                                                   equence 4, Application US/08442282 atent No. 5760204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                     5593 agtcctggctgtccttggaactcactctgtagaccaggctggccttgaactcagaaatcc 5652
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                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                   APPLICANT:
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STRANDEDNESS: 5...
linear
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COUNTRY:
                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US FILING DATE: 19910910 CLASSIFICATION: 530
                                                                ADDRESSEE:
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REGISTRATION NÜMBER: 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                 AGCTCTGGCTGTCC-TGGAACTCACTTTATAGACCAAGCTGGCCTCGAACTCAGAAATCC
                                                                                                                                                                                                  INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRY: U.S.A.
10036-2711
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                                                                                                                  INVENTION:
             New York
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                                              1155 Avenue of the Americas
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                                                                                                                                                               Tominaga,
                                                                                                                                Murata,
                                                                                                                                                Takagi,
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Tominaga, Akira
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55 Avenue of the Americas
                                                                  Pennie &
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, Yoshiyuki
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78.4%;
                                                                                                                Human And Murine Interleukin-5 Receptor
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                                                                Edmonds
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Best Local Similarity
Matches 159; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          quence 3, Application US/08555723B tent No. 5837534
                                                                         4000 tttggctcttggtaactgtcccagggcctctctgacacacagggttgtagccccagctcc 4059
                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 3892 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                              MOLECULE TYPE:
HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPUTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 800
TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington, D.C. STATE: D.C
                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: A-6663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 14-NOV
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LE OF INVENTION:
                       ttggctttttgagacagggtttctctgtacagccctggctgccctggcactcattctgta 4179
GCCTCCCGAGTGCTGGGATTAAAGGCATGCACCACCACCACCAGCA 3110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KIT, Gordon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: SUGHRUE, MION, ZINN, MACPEAK & SEAS 2100 Pennsylvania Avenue, N.W., Suite
                                                                                                                                                                                   Conservative
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293-7860
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                                                                                                                                                                                                 Score 100.2; DB / Pred. No. 6.1e-15
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THE SAME, AND METHOD O
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                                                                                                                                                                            Query Match 0.8%;
Best Local Similarity 82.5%;
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                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617) 876-585
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS
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4223 ttccagtgctggcacta 4239
                                                                                                             4103 tttttttcttttttttggctttttgagacagggtttctctgtacagccctggctgcc 4162
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APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                      459
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                                                                                                                                                                                                                                                                                                           TYPE: nucleic aci
                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
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CLASSIFICATION: 536
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                                                        TTTGTTGGGTTTTCGTTTTTGGTTTTTCGAGACAGGGTTTCTCTGTATAGCCCCTGGCTGTC
                               CTARAACTCACTCTGTAGACCAGGCTGGCCTCGAACTCAGAAATCTGCCCGCTTCTGCCT
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                                                                                                                                                                                                                                                                                                                        535 base pairs
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87 CambridgePark Drive
                                                                                                                                                               Conservative
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Spaulding, Vikki
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Treacy, Maurice
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876-5851
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                                                                                                                                                          Score 99.8; DE 2;
Pred. No. 2.6e-15;
1; Mismatches 23
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US-08-299-849B-5
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Best Local S
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4099 ttaatttttttttttttttttggctttttgagacagggtttctctgtacagccctggc 4158
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                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
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129; Conserv
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ICATION NUMBER: 9-JULY-1991
APPLICATION DATA:
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                                                                                                                                                                  : 4698 base pairs nucleic acid
                                                                                                                                                                                                                                                                                                                                           ATION NUMBER:
                                                                                                                                                                                                                                                                                                              DATE: 23-May
/AGENT INFORMA
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                                                                                                                                                                                                                                                                                                   Hanson,
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DATE: 23-SEPTEMBER-1991
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                                                                                                                    genomic DNA
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                               Score 111.6;
Pred. No. 1.1e
0; Mismatches
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                        1.1e-17;
29;
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    Query Match
Best Local Similarity
Matches 127; Conserv
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Patent No. 5574136
                                                                                                                                                                                                     INFORMATION FOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: JP 7
FILING DATE: 23-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                NAME: Hellwege, James W. REGISTRATION NUMBER: 28,808
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                              TRANDEDNESS:
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180..2690
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                     linear
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03-JUL-1990
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                                                                                                                                                                                                                                                                                                                                                                                                   JP 74539/1990
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Score 103.6; DB 1;
Pred. No. 8.2e-16;
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                           Length
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Result
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Copyright (c) 1993 - 1998 Compugen
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US-08-442-281-16

US-08-232-463-14

US-08-232-463-14

US-07-757-390-15

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US-08-442-282-2

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US-08-442-281-15

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US-08-487-748A-6

US-08-555-723B-4

US-08-380-403A-3

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US-08-380-09098-1
US-08-472-217-1
US-08-488-195-94-4
US-08-465-794-4
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US-08-608-23-1
US-08-290-731C-3
US-08-22-177A-8
US-08-291-587A-1
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                 ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 70
                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                           FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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LECOMMUNICATION INFORMATION:
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10036-2711
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Murata, Yoshiyuki
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Pred. No. 1.6e-13;
                 7005-030
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Best Local Similarity
Matches 122; Conserv
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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WHORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                MOLECULE TYPE: DNA (genomic)
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                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                               NAME: Misrock, S. Leslie REGISTRATION NUMBER: 18,
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   LOCATION:
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                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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Tominaga, Akira
                                                                   linear
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Yoshiyuki
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Query Match
0.8%; Score 94.2; DB 3; Length 1808;
Best Local Similarity 80.8%; Pred. No. 1.2e-13;
Matches 122; Conservative 0; Mismatches 28; Indels 1; Gaps
0; 5549 gtttggttttgagttttgtttatttgagacagggcttctctgtgtagtcctggctgtcctt 5608
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; TOPOLOGY: 11;
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US-08-442-282-2
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Best Local Similarity 80.8
Matches 122; Conservative
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NFORMATION FOR SEQ ID NO:
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                                                                                           SEQUENCE CHARACTERISTICS:
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                                            STRANDEDNESS:
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                                                                                                                                                        TELEPHONE:
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                                                                                                                                                         ELEPHONE: 212 790-9090
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                                                                                                                                                                                                                                                     PPLICATION NUMBER: 07/7
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                                                                         1808 base pairs
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Tominaga, Akira
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YSTEM: PC-DOS/MS-DOS
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Pred. No. 1.2e-13;
); Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                            Version #1.25
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Search completed: September 19, 1999, 16:09:05 Job time: 16199 sec

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A1670108.1
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242; Conservative
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                                                  A1670108 385 bp mRNA we655703.x1 Soares_thymus_NHFTh Homo sapiens or IMAGE:2345981 3' similar to TR:075462 075462 PRECURSOR.; mRNA sequence.
                                   g4834882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 407.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg,
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
On Jan 14, 1998 th
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Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         double-Stranded CDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatina Bonaldo. This library was constructed from the same fetus as the fetal heart library. Soares fetal heart NbHHJ9W."

169 c 122 g 72 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Soares_fetal_lung_NbHL19W"
/dev_stage="19 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strand CDNA was primed with a Not I - oligo(dT) primer [5.-IGTTACCAATTTTTTTTTTT-3']
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/db_xref="taxon:9606"
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                  GI:4834882
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Pred. No. 1.7e-37;
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                                                                                    cDNA clone
2 CYTOKINE-LIKE FACTOR-1
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Best Local Similarity
Matches 240; Conserv
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W66776 482 bp mRNA EST 14-JUN-1996 mel7bl1.rl Soares mouse embryo MbME13.5 14.5 Mus musculus cDNA clone IMAGE:387741 5' similar to pIR:H38252 B38252 granulocyte colony-stimulating factor receptor precursor; mRNA sequence. W66776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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On May 9, 1996 thi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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1 (bases 1 to 385)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B (phage-resistant)"
/note="Organ: thymus, pooled; Vector: pT7T3D-Pac
/Pharmacia, with a modified polylinker; Site_1: |
Site_2: Eco RI; 1st strand cDNA was primed with |
oligo(dT) primer [5'
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/dev_stage="fetal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 215.4; DB 50;
Pred. No. 1.1e-36;
D; Mismatches 41;
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197
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                                                                                           ctgagtgtgcgctgggtctcaccaccagctctcaaggatttcctcttccaagccaagtac 8723
                                cag-atccgctaccgcgtggaggacagcgtggactggaaggtgcccgtcccgccccggac 8782
                                                                     CTGAGTGTGCGCTGGGTCTCACCACCAGCTCTCAAGGATTTCCTCTTCCAAGCCAAGTAC
                                                                                                                                                   GTGACCACGGACCCCCACCCGACGTGCACGTGAGCCGCGTTGGGGGGCCTGGAGGACCAG
                                                                                                                                                                                                                                    305;
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WashUrHHMI Mouse EST project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g1375694
W66776.1
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Email: mouseestavailable royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuc
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1996
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/dev_stage="13.5-14.5dpc
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                                                                                                                                                                                                                                                                             Thermostabilization and thermonctivation of thermolabile enzymes | trehalose and its application for the synthesis of full length cDI (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
                                                                                                                                                                                                                                                                                                                                                                                                      3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Tel: 81-298-36-9145
Fax: 81-298-36-9098
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On Jun 22, 1
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AV032198 Mus musculus adult C57BL/6J cerebellum
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/clone="1500034F20"
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/strain="C57BL/6J"
                                                                                           /clone_lib="Mus musculus adult C57BL/6J cerebellum"
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Query Match

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13587.681 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

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WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The WashU-HHMI Mouse EST Project Unpublished (1996)
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Marra, M., Hillier, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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house mouse.
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                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="raxon:10090"
/clone="IMAGE:474733"
/clone_lib="Soares mouse embryo NbME13.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'dev_stage="13.5-14.5dpc total fetus"
'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'tissue_type="embryo"
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Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                  2.1%;
                                                                                                                                                                                                                                                                                                                 Pred. No. 9.4e-44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 462)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/ONINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index (CGAP/BTGAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Feb 17, 1998 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert Length: 1631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Lou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 462)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence stop: 454
                                                                                                                              79
                                                                                                                      T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

181 c 122 g 79 t 1 others
                                                                                                                                                                                                                                                /clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE: 2105495"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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                     1.9%;
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Score 221.8; DB of Pred. No. 4.7e-38; O; Mismatches 3:
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                                        Length
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                                                                                                                                                                                                                                                                                                                                                                                                                               Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 474)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurolk Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)

On Apr 7, 1998 this sequence version replaced g1:3034955
                                                                                                                                                                                                                                                                                                                                                                     Insert Length: 1664
Seq primer: -40UP f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue Procurement:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Robert_Strausberg@nih.gov
the Not I and Eco RI sites of the modified Library is normalized, and was constructed Soares and M.Fattima Bonaldo."

181 c 128 g 83 t 1 others
                                                                                                         adaptors (Pharmacia),
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'db_xref="taxon:9606"
                                                                                                                                                                                       lone="IMAGE: 2097265"
lone_lib="NCI_CGAP_Brn23"
issue_type="glioblastoma (pooled)"
ab_host="DH10B"
                             double-stranded cDNA was ligated to Eco RI s (Pharmacia), digested with Not I and cloned into I and Eco RI sites of the modified pT7T3 vector. Is normalized, and was constructed by Bento
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National Cancer Institute, Cancer Genome Anat
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IMAGE:1705398
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Robert_Strausberg@nih.gov
                                                   /dev_stage="19 weeks //lab_host="DHIOB (ampicillin resistant)" //lab_hos
double-stranded cDNA was size selected, adapters (Pharmacia), digested with Not the Not I and Eco RI sites of a modifie
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normalization to a Cot - 5. Library constructed by M.Fatima Bonaldo. This library was constructed from same fetus as the fetal lung library, Soares fetal NbHL19W."
                                                                /clone="IMAGE:1741879"
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                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert-Strausberg@nih.gov
This clone is available royalty-f
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                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Verte Eutheria; Primates; Catarrhini; Hominidae; HC 1 (bases 1 to 47) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.National Cancer Institute, Cancer Genome Anat Tumor Gene Index
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                                                                                                                                                                  IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1552 Std Error: 0.00
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1742408"
/clone_lib="Soares_fetal_lung_NbHL19w"
/dev_stage="19 weeks"
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1667 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 431.
                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
On Aug 21, 1998 th
                                                                                                                                                    Contact: Robert Strausberg, Ph.D
Tel: (301) 496-1550
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                          Email: Robert_Strausberg@nih.gov
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National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 417)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Pro
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.linl.gov) for further i
Insert Length: 1634 Std Error: 0.00
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Unpublished (1997)
On Aug 21, 1998 this sequence version
                                                                       Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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175 c 128 g 74 t 1 others
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                                                                Genome Res. 6 (9),
97044477
                                                                                                                           Eutheria; Rodentia;
1 (bases 1 to 332)
Bonaldo, M.F., Lennon
                                                                                                                                                                                          Rattus norvegicus
                                                                                                                                                                                                                                                                                 AI579568 332 bp mRNA
UI-R-GO-ut-h-08-0-UI.S3 UI-R-GO Rattus
UI-R-GO-ut-h-08-0-UI 3', mRNA sequence.
                                                 On Mar 10,
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                                                                                                 discovery
                                                                                                           Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two appr
                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                            Norway rat.
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   for Rat
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/lab_host="DH10B"
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/tissue_type="Pooled human me
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Location/Qualifiers
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Sciurognathi; Muridae; Murinae;
 Discovery
                                               sequence version
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Pred. No. 1e-37;
D; Mismatches
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Mapping
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cDNA clone
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Rattus.
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                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 431)
                                                                                                                                                                                                              AI333812 431 bp mRNA EST qp93e12.x1 Soares_fetal_lung_NbHL19W Homo sai MAGE:1930806 3' similar to TR:Q16354 Q16354
  1 (bases 1 to 431)
NCI-CGAP http://www
                                                                                                                                                           g4070371
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451 Eckstein Medical Research Building Iowa City, IA 522
451 Eckstein Medical Research Building Iowa City, IA 522
Tel: 319 335 8250
Fax: 319 33 9565
Email: msoares@blue.weeg.ulowa.edu
Digo-dT track not found, Not I site shown in beginning
is likely internal to the message. cDNA Library Preparat
Soares Lab Clone distribution: clones will be available
                                                                           Homo sapiens
                                                                                                                                                                                                mRNA sequence.
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Seq primer: M13 Forward.
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/lab_host="DHIOB (Life Technologies)"
/lab_host="DHIOB (Tife Technologies)"
/lab_host="DHIOB (Pharmacia) with a modified
/note="Vector: pi7T3D-Pac (Pharmacia) with a modified
/polylinker; Site_1: Not I; Site_2: Ecc RI; The UI-R-G0
// library is a normalized library constructed from a
mixture of rat tissues (nodose ganglia, dorsal root
// ganglia, and trigeminal ganglia). The tag is a string of
// functeotides present between the Not I site and the
// oligo-dT track. The library was constructed as described
// by Bonaldo, Lennon and Soares, Genome Research 6:
// 1806, 1996."
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/strain="Sprague-Dawlay"
/db_xref="taxon:10116"
/clone="UI-R-GO-ut-h-08-0-UI"
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.ncbi.nlm.nih.gov/ncicgap
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Bonaldo, M.F., Lennon
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UI-R-G0-uc-b-11-0-UI.s1
UI-R-G0-uc-b-11-0-UI 3',
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Seq primer: M13 Forward.
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/lab_host="DHIOB (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-G0 library is a normalized library constructed from a mixture of rat tissues (nodose ganglia, dorsal root ganglia, and trigeminal ganglia). The tag is a string
                                                                                                                                                                                                                                                                                                                                             Soares, MB
for Rat Gene Discovery and Mapping
                                                                                                                                         /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                               /map="6p21.3; 5q33"
/clone="UI-R-G0-uc-b-11-0-UI'
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Rodentia; Sciurognathi; Muridae; Murinae;
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mb75b01.rl soares mouse
IMAGE:335209 5', mRNA se
W17583
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W17583.1
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Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free t)
IMAGE Consortium (info@image.llnl.gov)
                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1996)
On May 9, 1995 thi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 390)
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                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
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/clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT7T3D (Pharmacia) with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by Bonaldo, Le
791-806, 1996
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                                                                                      /clone="IMAGE:335209"
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Pred. No. 6.
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        (Pharmacia) with a modified
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v) for further
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                       11713 cccagtg--tgggtagggttggggtattgcaggggctccccaagagtctctt 11761
                                                                                                                                                                                                                                                                                                                                  11534 aggtcctgccggctaaactctaaggataggccatcctcctgctgggtcagacctggaggc 11593
                                                                                                                                                                                                                                 11594 tcacctgaattggagcccctctgtaccatctgggcaacaaagaaacctaccagaggct-g 11652
                                                                                                                             11653 ggcacaatgagctcccacaaccacagctttggtccacatgatggtcacacttggatatac 11712
340 CCCAGTGGTGAGGGTTGGGGTATTGCAGGGCCTCCCAAGAGTCTCTT 390
                                                                                                                                                                                                    220 TCACCTGAATTGGAGCCCCTCTGTACCATCTGGGCAACAAAGAAACCTACCAGAGGCTGG 279
                                                                                                                                                                                                                                                                                                     160 AGGTCCTGCCGGCTAAACTCTAAGGATAGGCCATCCTCCTGCTGGGTCAGACCTGGAGGC 219
                                                                                                   280 GGCACAATGAGCTCCCACAACCACAGCTTTGGTCCACATGATGGTCACACTTGGATATAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through odi round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. RNA was kindly provided by
Dr. Minoru Ko (Wayne State University)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                 ctgctctatacatggagacacacctggggccaccgctgaggggctctactggaccttcaa 6450
                                                                                                                                                                                                                                                               CCTGGCCAACCTCAATGGGTCCAGGCAGCGGTCGGGGGACAACCTCGTGTGCCACGCCCG
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                                                                                                                                                                                                TGACGGCAGCATCCTGGCTGGCTCTCTATGTTGGC
                                                              AI670108 385 bp mrNA
we65f03.x1 Soares_thymus_NHFTh Homo sapiens cDNA clone
iMAGE:2345981 3'...similar to TR:075462 075462 CYTOKINE-LIKE FACTOR-1
                                               PRECURSOR. ;, mRNA
AI670108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) On Jan 14, 1998 this sequence version replaced g1:1797892.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1615 Std Error: 0.00
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Email: Robert_Straus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Soares_fetal_lung_NbHL19W"
/dev_stage="19 weeks"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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               GI:4834882
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RESULT 1 W66776/c

DEFINITION

W66776 482 bp mRNA EST 14-JUN-1996 mel/Dbl1.rl Soares mouse embryo NbMEl3.5 14.5 Mus musculus cDNA clone IMAGE:387741 5' similar to PIR:B38252 B38252 granulocyte colony stimulating factor receptor precursor; mRNA sequence. W66776

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ACCESSION

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Best Local Similarity
Matches 240; Conserv
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                                                                                                                                      ACGGGCGCCCCCCCCCCGAGCTCTCCCCGTGTACTCAACGCCTCCACCTTGGCTCTGG
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                                                   GTGAC
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1 (bases 1 to 385)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project Tumor Gene Index
Unpublished (1997)
On May 9, 1996 this sequence version replaced gi:1133091.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: Robert_Strausberg@nih.gov
This clone is available royalty-free the IMAGE Consortium (info@image.llnl.gov)
Seq primer: -40UP from Gibco
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Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                 PARCATCTIGGCTGGCTCCTGGCCTTATGTTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the and Eco RI sites of the modified pT773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. a 156 c 108 g 66 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Soares_thymus_NHFTh"
/dev_stage="fetal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                        1.8%;
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Pred. No. 1.1e-35;
0; Mismatches 41;
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KEYWORDS
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Best Local Similarity
Matches 305; Conser
                                                                                                        8664 ctgagtgtgcgctgggtctcaccaccagctctcaaggatttcctcttccaagccaagtac 8723
                                                                                                                                                                                                   8604 gtgaccacggaccccccacccgacgtgcacgtgagccgcgttgaggggcctggaggaccag 8663
                                                                                                                                                                      317 GTGACCACGCACCCCACCCGACGTGCACGTGAGCCGCGTTGGGGGGCCTGGAGGACCAG
                                                                                    257
                      CAGTATTCGCTACCGCGTGGAGGACAGCGTGGACTGGA------
                                                                                    CTGAGTGTGCGCTGGGTCTCACCACCAGCTCTCAAGGATTTCCTCTTCCAAGCCAAGTAC
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W66776.1
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On Apr 14, 1993 this sequence version replaced gi:785250
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1 (bases 1 to 482)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              possible reversed clone: similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1444 Forest Park Parkway, Box 8501,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     his clone is available royalty-free through LLNL; contact the NAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                              96
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                                                                                                                                                                                                                                                                                                                                                                                     Eco RI adaptors (Pharmacia), digested with Not I and Cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo.

a 138 c 147 g 101 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
'strain="C57BL/6J"
'db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         issue_type="embryo"
ev_stage="13.5-14.5dpc total fetus"
ab_host="DH10B"
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Pred. No. 1.6e-36;
0; Mismatches 2
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Unpublished (1999)
On Jun 22, 1998 this sequence version replaced gi:3246782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Ito,M., Aizav
Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,
Hara,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Science Laboratory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M. Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H.,
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                                                                                                                                                                                                                                                                    further details.
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                                                                                                                                                                                                                                                                                     Please visit our web site (http://genome.rtc.riken.go.jp)
                                                                                                                                                                                                                                                                                                                                                        rehalose and its application for the synthesis of f (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
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el: 81-298-36-9145
                                                                                                                                                                                                                                                                                                                                                                                                                            mail: genome-res@rtc.riken.go.jp
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lone 1500034F20, mRNA
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                       63
                                                                                                                             /db_xref="taxon:10090"
/clone="1500034F20"
                       /dev_stage="adult"
63 c 69 g
                                                                                      /clone_lib="Mus musculus adult C57BL/6J cerebellum"
/sex="male"
                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
                                                            'tissue_type-"cerebellum"
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Query Match

1.8%;

Score 213;

DB 50;

Length 262

(GENE-) GENETICS IN (WHIT-) WHITEHEAD I D'andrea A, Wong G; WPI; 90-260931/34.

INC

N-PSDB; Q05748.

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        recombinant EPO receptor produced on expression of the DNA are used to develop reagents and systems to control and study erythropolesis. It is believed that the EPO receptor is dysfunctional in individuals with Diamond Blackfan anaemia, and make also R06511 (murine EPO receptor).

Sequence 508 AA;
        Example: Fig 12: 24pp; German.

The sequence is that of fusion protein GM-CSFRFc comprising the extracellular domain of granulocyte macrophage-colony stimulating factor (GM-CSF) fused via a hinge region to the Fc part of the heavy chain of human IgGl. It may be used as part of a cell free receptor binding test which can be used for the identification of agonists, antisodies, biological activity of soluble cellular receptors, functional analysis of modified ligands and diagnostic or therapeutic substances. See also R24016.
                                                                                                                                     WPI; 92-185084/23. Cell free receptor binding test contg. recombinant fusion protein comprising carrier bound to fusion partner coupled to fixed support and second, labelled binding partner, for receptor or antibody
                                                                                                                                                                                                                                         EP-488170-A.
03-JUN-1992.
26-NOV-1991; 120187.
28-NOV-1990; DE-037837
                                                                                                                                                                                                                                                                                                                                                                                                                                        Fusion protein GM-CSFRFc. Granulocyte macrophage-colony immunoglobulin G1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Erythropoietin receptor and gene - used for developing reagents and systems to control and study erythropolesis. Disclosure, Fig 2, 53pp, English.

The sequence was deduced from DNA obtd. from a clone isolated fi a commercially available human geenomic cDNA library in phage Lambda Fix (Stratagene). The sequence encodes a type I transmembrane protein with binding affinity for EPO. The gene and
                                                                                                                                                                                               (BEHW) BEHRINGWERKE AG.
Lauffer L, Oquendo P, Zettlmeissl
WPI; 92-185084/23.
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                                                                                                                                                                                                                                                                                                                                                                                  "human GM-CSF receptor"
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Query Match

96

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                                                                                                                                                                                                                                                                                                                              Disclosure; Fig. 1 (A-E); 11pp; English.

CC The human PRL receptor cDNA is isolated by screening a lambda gt 10

CC library prepared from normal human hepatoma Hep G2 and T47-D breast

CC cancer cells. Initially, 1x10 6 recombinants are screened with the

CC control probe: a complementary RNA of the F3 cDNA of the rat

CC prolactin receptor. One positive recombinant was isolated from the

CC prolactin receptor. One positive recombinant was isolated from the

CC prolactin receptor. One positive recombinant was isolated from the

CC prolactin receptor. One positive recombining two of the six cDNAs, a PRL receptor cDNA of 2.5 kb was constructed,

CC contg. a single ONF of 1866 bp. Similar partial length cDNA were

CC isolated from the T47-D library.

CC contg. a single ONF of 1866 bp. Similar partial length cDNA were

CC isolated from the T47-D library.

CC several regions of sequence identity between the human growth

CC several regions of sequence identity between the human growth

CC several regions of sequence identity between the human growth

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CC used for the screening of growth hormone variants, for the development

CC used for the screening of growth hormone variants, for the development

CC cancer biopsies, for the measaurement of bioactive forms of prolactin,

CC the immune system
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Best Local S
Matches 4
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16-DEC-1988; 286445.
16-DEC-1988; US-2864
(ROYA-) ROYAL INST #
                         08-MAY-1991 (first entry)
Humam GM-CSF receptor.
Granulocyte-macrophage colony-stimulating
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WPI; 91-065341/09.

Isolated CDNA sequence incoding human prolactin receptor - useful for expressing the receptor, e.g. for screening assays and antibody
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Human prolactin receptor; PRL;
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44

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810 218

R04574 W40287

Derived amino acid Human TSP1 protein

ALIGNMENTS

Result No. Perfect score: Sequence:

US-09-037-657-1 31 1 WSXWS 5

BLOSUM62

Scoring table: Searched:

Pred.

A\_Geneseq\_36:\*

188963 segs, 23686106 residues

No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed. s derived by analysis of the total score distribution.

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GenCore version Copyright (c) 1993 - 1998

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Score Match Length 1522 1522 1522 1522 1584 DB Aeromonas caviae x
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